

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 09:47:41 ; Search time 68.2273 Seconds
(without alignments)
455.672 Million cell updates/sec

Title: US-09-542-718-2

Perfect score: 19
Sequence: 1 aacggcagcgcttcttgc 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/1/ina/5A-COMB.seq:
2: /cgn2_6/prodata/1/ina/5B-COMB.seq:
3: /cgn2_6/prodata/1/ina/6A-COMB.seq:
4: /cgn2_6/prodata/1/ina/6B-COMB.seq:
5: /cgn2_6/prodata/1/ina/PCTUS-COMB.seq:
6: /cgn2_6/prodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	US-09-973-132-2	Sequence 2, Appli
2	19	100.0	106	US-09-973-132-1	Sequence 1, Appli
3	19	100.0	1242	PCT-US91-00909-3	Sequence 3, Appli
4	19	100.0	2305	US-09-016-434-1282	Sequence 1282, Ap
5	19	100.0	2305	US-09-023-655-1249	Sequence 1249, Ap
6	19	100.0	3451	US-09-811-286-1	Sequence 1, Appli
7	19	100.0	5857	US-09-293-170-4	Sequence 4, Appli
8	16.4	86.3	482	US-09-640-211A-108	Sequence 108, App
9	16.4	86.3	1194	US-09-902-540-5572	Sequence 5572, Ap
10	16.4	86.3	41927	US-09-902-540-1268	Sequence 1268, Ap
11	16.4	86.3	4403765	US-09-103-840A-2	Sequence 2, Appli
12	15.8	83.2	336	US-09-252-991A-28	Sequence 28, Appli
13	15.8	83.2	1584	US-09-351-223-1	Sequence 1, Appli
14	15.8	83.2	1828	US-09-902-540-3724	Sequence 3724, Ap
15	15.8	83.2	3334	US-09-086-663A-1	Sequence 1, Appli
16	15.8	83.2	6178	US-09-086-663A-72	Sequence 72, Appli
17	15.8	83.2	12173	US-09-902-540-1022	Sequence 1022, Ap
18	15.8	83.2	24656	US-09-949-016-15575	Sequence 15575, A
19	15.8	83.2	536165	US-09-214-808-1	Sequence 1, Appli
20	15.4	81.1	289	US-09-313-294A-6802	Sequence 6802, Ap
21	15.4	81.1	939	US-09-134-000C-2802	Sequence 2802, Ap
22	15.4	81.1	1400	US-08-001-078A-2	Sequence 2, Appli
23	15.4	81.1	1400	US-08-463-218-2	Sequence 2, Appli
24	15.4	81.1	1400	PCT-US94-0023-2	Sequence 2, Appli
25	15.4	81.1	1482	US-08-660-645A-6	Sequence 6, Appli
26	15.4	81.1	1482	US-09-298-718-6	Sequence 6, Appli
27	15.4	81.1	1482	US-09-546-969-6	Sequence 6, Appli

28	15.4	81.1	1482	4	US-09-547-267-6	Sequence 6, Appli
29	15.4	81.1	1752	4	US-09-489-039A-6747	Sequence 6747, Ap
30	15.4	81.1	1959	4	US-09-949-016-4614	Sequence 4614, Ap
31	15.4	81.1	2415	4	US-09-270-767-15185	Sequence 15185, A
32	15.4	81.1	6414	3	US-09-134-001C-1626	Sequence 1626, Ap
33	15.4	81.1	8625	3	US-08-980-832-1	Sequence 1, Appli
34	15.4	81.1	8625	4	US-09-920-923B-1	Sequence 27, Appli
35	15.4	81.1	11233	3	US-08-980-832-27	Sequence 27, Appli
36	15.4	81.1	11233	4	US-09-920-923B-27	Sequence 27, Appli
37	15.4	81.1	84171	4	US-09-949-016-16356	Sequence 16356, A
38	15	78.9	238	4	US-09-640-211A-155	Sequence 155, App
39	15	78.9	407	4	US-09-640-211A-1769	Sequence 1769, Ap
40	15	78.9	470	4	US-09-640-211A-1779	Sequence 1779, Ap
41	15	78.9	561	4	US-09-640-211A-1719	Sequence 1719, Ap
42	15	78.9	687	4	US-09-902-540-6577	Sequence 6577, Ap
43	15	78.9	1027	4	US-09-602-787A-293	Sequence 293, App
44	15	78.9	1140	4	US-09-602-787A-291	Sequence 291, App
45	15	78.9	1347	4	US-09-896-621B-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-973-132-2
; Sequence 2, Application US/09973132
; Patent No. 6593092
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687.US.P1
; CURRENT APPLICATION NUMBER: US/09/973,132
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragments
US-09-973-132-2

Query Match 100.0%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AACGGCAGCGCTTCTTGC 19
|||
Db 1 AACGGCAGCGCTTCTTGC 19

RESULT 2
US-09-973-132-1
; Sequence 1, Application US/09973132
; Patent No. 6593092
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687.US.P1
; CURRENT APPLICATION NUMBER: US/09/973,132
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 106
; TYPE: DNA

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragment
US-09-973-132-1

Query Match 100.0%; Score 19; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGCAGCGCTTCTTGC 19
Db 1 AACGGCAGCGCTTCTTGC 19

RESULT 3

PCT-US91-00909-3
; Sequence 3. Application PC/TUS9100909
; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej Z.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Methods of Producing Hybrid G
; TITLE OF INVENTION: Protein-Coupled Receptors
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: United States
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00909
; FILING DATE: 19910208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.408PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1242 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1242
PCT-US91-00909-3

Query Match 100.0%; Score 19; DB 5; Length 1242;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGCAGCGCTTCTTGC 19
Db 16 AACGGCAGCGCTTCTTGC 34

RESULT 4

US-09-016-434-1282
; Sequence 1282, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1282:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 929370
US-09-016-434-1282

Query Match 100.0%; Score 19; DB 4; Length 2305;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGCAGCGCTTCTTGC 19
Db 809 AACGGCAGCGCTTCTTGC 827

RESULT 5

US-09-023-655-1249
; Sequence 1249, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1249:
SEQUENCE CHARACTERISTICS:
LENGTH: 2305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 929370
US-09-023-655-1249

Query Match 100.0%; Score 19; DB 4; Length 2305;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGCAGCGCCTTCTTGC 19
|||||
DB 809 AACGGCAGCGCCTTCTTGC 827

RESULT 6

US-09-811-286-1
Sequence 1, Application US/09811286
Patent No. 6586183
GENERAL INFORMATION:
APPLICANT: Drysdale, Connie M
APPLICANT: Judson, Richard S
APPLICANT: Liggett, Stephen B
APPLICANT: Nandabalan, Krishnan
APPLICANT: Stack, Catherine B
APPLICANT: Stephens, J. Claiborne
TITLE OF INVENTION: Association of beta2-adrenergic receptor haplotypes
FILE REFERENCE: with drug response
CURRENT APPLICATION NUMBER: US/09/811,286
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 3451
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1588)..(2829)
US-09-811-286-1

Query Match 100.0%; Score 19; DB 4; Length 3451;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGCAGCGCCTTCTTGC 19
|||||
DB 1603 AACGGCAGCGCCTTCTTGC 1621

RESULT 7

US-09-293-170-4
Sequence 4, Application US/09293170
Patent No. 6383777
GENERAL INFORMATION:
APPLICANT: Breyer, Richard M.
APPLICANT: Ma, Lijun
APPLICANT: Kennedy, Chris
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH YIELD
PRODUCTION OF EUKARYOTIC PROTEINS
FILE REFERENCE: 22000.0094
CURRENT APPLICATION NUMBER: US/09/293,170
CURRENT FILING DATE: 1999-04-16
EARLIER APPLICATION NUMBER: 60/081,989
EARLIER FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 5857
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (300)...(1799)
OTHER INFORMATION: Description of Artificial Sequence:/note =
OTHER INFORMATION: synthetic construct
US-09-293-170-4

Query Match 100.0%; Score 19; DB 3; Length 5857;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGCAGCGCCTTCTTGC 19
|||||
DB 549 AACGGCAGCGCCTTCTTGC 567

RESULT 8

US-09-640-211A-108
Sequence 108, Application US/09640211A
Patent No. 6833446
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Sherk, Michael A.
APPLICANT: McGrath, Amette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 108
LENGTH: 482
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-09-640-211A-108

Query Match 86.3%; Score 16.4; DB 4; Length 482;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ACGGCAGCGCCTTCTTGC 19
|||||
DB 339 ACGGCATCGCCTTCTTGC 356

RESULT 9

US-09-902-540-5572/c
Sequence 5572, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:

```
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5572
; LENGTH: 1194
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5572

Query Match      86.3%; Score 16.4; DB 4; Length 1194;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AACGGCAGCGCTTCTTG 18
Db      680 AACGGCAGCGCTTCTTG 663

RESULT 10
US-09-902-540-1268/c
; Sequence 1268, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1268
; LENGTH: 41927
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1268

Query Match      86.3%; Score 16.4; DB 4; Length 41927;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AACGGCAGCGCTTCTTG 18
Db      6836 AACGGCAGCGCTTCTTG 6819

RESULT 11
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match      86.3%; Score 16.4; DB 3; Length 4403765;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 ACGGCGCGCTTCTTGC 19
Db      2266582 ACGGCGCGCTTCTTGC 2266565

RESULT 12
US-09-252-991A-28/c
; Sequence 28, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Maic J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 28
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28

Query Match      83.2%; Score 15.8; DB 4; Length 336;
Best Local Similarity 89.5%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AACGGCAGCGCTTCTTGC 19
Db      110 AACGGCAGCGCTTCTTGC 92

RESULT 13
US-09-351-229-1/c
; Sequence 1, Application US/09351229
; Patent No. 6380465
; GENERAL INFORMATION:
; APPLICANT: Barrett, Michael
; TITLE OF INVENTION: Cytochrome P450 Enzymes and Related Compounds and.
; FILE REFERENCE: P-1049
; CURRENT APPLICATION NUMBER: US/09/351,229
; CURRENT FILING DATE: 1999-07-11
; EARLIER APPLICATION NUMBER: 60/092,596
; EARLIER FILING DATE: 1998-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1584
; TYPE: DNA
; ORGANISM: Zea mays
US-09-351-229-1

Query Match      83.2%; Score 15.8; DB 3; Length 1584;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
```

Search completed: August 7, 2005, 11:52:13
Job time : 75.2273 secs

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AACGGCAGCGCTTCTTGC 19
Db 245 AGCGGCAGCGGCTTCTTGC 227

RESULT 14
US-09-540-3724/c
; Sequence 3724, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3724
; LENGTH: 1828
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-540-3724

Query Match 83.2%; Score 15.8; DB 4; Length 1828;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AACGGCAGCGCTTCTTGC 19
Db 1764 ACCGCCAGCGCTTCTTGC 1746

RESULT 15
US-09-086-663A-1/c
; Sequence 1, Application US/09086663A
; Patent No. 6518063
; GENERAL INFORMATION:
; APPLICANT: DUCY, PATRICIA
; APPLICANT: KARSENTY, GERARD
; TITLE OF INVENTION: OSF2/CBP1 COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: UTSC:525
; CURRENT APPLICATION NUMBER: US/09/086,663A
; CURRENT FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/080,189
; PRIOR FILING DATE: 1998-03-24
; PRIOR APPLICATION NUMBER: 60/048,430
; PRIOR FILING DATE: 1997-05-29
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3334
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-086-663A-1

Query Match 83.2%; Score 15.8; DB 4; Length 3334;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AACGGCAGCGCTTCTTGC 19
Db 190 AACGCCAGCGCTTCTTGC 172

This Page Blank (uspto)

```

Query Match      100.0%; Score 19; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGCAGCGCCTTCTTGC 19
    |||||
Db 1 AACGGCAGCGCCTTCTTGC 19
    |||||

```

RESULT 2
US-09-973-132-1
; Sequence 1, Application US/09973132
; Publication No. US20020137069A1
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; APPLICANT: Merchant, B.T.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687.US.P1
; CURRENT APPLICATION NUMBER: US/09/973,132
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 106
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragment
US-09-973-132-1

Query Match 100.0%; Score 19; DB 9; Length 106;
Best Local Similarity 100.0%; Pred. No. 7.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGCAGCGCCTTCTTGC 19
|||||

Db 1 AACGGCAGCGCCTTCTTGC 19
|||||

RESULT 3
US-10-321-039-28
; Sequence 28, Application US/10321039
; Publication No. US20040014067A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kurensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (561)..(561)
; OTHER INFORMATION: n can be a or g.
US-10-321-039-28

Query Match 100.0%; Score 19; DB 17; Length 1021;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGCAGCGCCTTCTTGC 19
|||||

Db 531 AACGGCAGCGCCTTCTTGC 549
|||||

RESULT 4
US-10-321-039-29
; Sequence 29, Application US/10321039
; Publication No. US20040014067A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kurensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (561)..(561)
; OTHER INFORMATION: n can be c or t.
US-10-321-039-29

Query Match 100.0%; Score 19; DB 17; Length 1021;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGCAGCGCCTTCTTGC 19
|||||

Db 86 AACGGCAGCGCCTTCTTGC 104
|||||

RESULT 5
US-09-993-844-9
; Sequence 9, Application US/09993844
; Patent No. US20020106739A1
; GENERAL INFORMATION:
; APPLICANT: Oakley, Robert H.
; APPLICANT: Barak, Lawrence S.
; APPLICANT: Laporte, Stephanie A.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Modified G-Protein Coupled Receptors
; FILE REFERENCE: 033072-026
; CURRENT APPLICATION NUMBER: US/09/993,844
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,772
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/260,363
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of beta2AR-V2R chimera
US-09-993-844-9

Query Match 100.0%; Score 19; DB 9; Length 1113;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGCAGCGCCTTCTTGC 19
|||||

Db 16 AACGGCAGCGCCTTCTTGC 34
|||||

RESULT 6
US-11-026-435-9
; Sequence 9, Application US/11026435
; Publication No. US20050106623A1
; GENERAL INFORMATION:
; APPLICANT: Oakley, Robert H.
; APPLICANT: Barak, Lawrence S.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Modified G-Protein Coupled Receptors
; FILE REFERENCE: 033072-026
; CURRENT APPLICATION NUMBER: US/11/026,435
; PRIOR FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: US/09/993,844
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,772
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/260,363
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; TYPE: DNA
; LENGTH: 1113
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of beta2AR-V2R chimera
US-11-026-435-9

Query Match 100.0%; Score 19; DB 23; Length 1113;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGCAGCGCCTTCTTGC 19
|||||

Db 16 AACGGCAGCGCCTTCTTGC 34
|||||

RESULT 7
US-09-935-061-5
; Sequence 5, Application US/09935061
; Publication No. US20030129649A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian M.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to G protein-coupled receptors
; FILE REFERENCE: STAN213
; CURRENT APPLICATION NUMBER: US/09/935,061
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(1239)
US-09-935-061-5

Query Match 100.0%; Score 19; DB 10; Length 1239;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGCAGCGCCTTCTTGC 19
|||||

Db 16 AACGGCAGCGCCTTCTTGC 34
|||||

RESULT 8
US-09-935-061-7
; Sequence 7, Application US/09935061
; Publication No. US20030129649A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian M.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to G protein-coupled receptors
; FILE REFERENCE: STAN213
; CURRENT APPLICATION NUMBER: US/09/935,061
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 2nd
; OTHER INFORMATION: Intracellular loop
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(1239)
US-09-935-061-7

Query Match 100.0%; Score 19; DB 10; Length 1239;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGCAGCGCCTTCTTGC 19
|||||

Db 16 AACGGCAGCGCCTTCTTGC 34
|||||

RESULT 9
US-10-692-071-5
; Sequence 5, Application US/10692071
; Publication No. US20040157268A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian K.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to membrane spanning, signal-transducing proteins
; FILE REFERENCE: STAN-213CIP
; CURRENT APPLICATION NUMBER: US/10/692,071
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: PCT/US02/13250
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/935,061
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(1239)
US-10-692-071-5

Query Match 100.0%; Score 19; DB 19; Length 1239;

Best Local Similarity 100.0%; Pred. No. 7.4; DB 19; Length 1242;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGCAGCGCTTCTTGC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 16 AACGGCAGCGCTTCTTGC 34

RESULT 10
US-10-692-071-7
; Sequence 7, Application US/10692071
; Publication No. US20040157268A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian K.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to membrane spanning, signal-transducing proteins
; FILE REFERENCE: STAN-213CIP
; CURRENT APPLICATION NUMBER: US/10/692,071
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: PCT/US02/13250
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/935,061
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 2nd
; OTHER INFORMATION: Intracellular loop
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-10-692-071-7

Query Match 100.0%; Score 19; DB 19; Length 1239;
Best Local Similarity 100.0%; Pred. No. 7.4; DB 19; Length 1239;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGCAGCGCTTCTTGC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 16 AACGGCAGCGCTTCTTGC 34

RESULT 11
US-10-221-332A-1
; Sequence 1, Application US/10221332A
; Publication No. US20040192625A1
; GENERAL INFORMATION:
; APPLICANT: University of Cincinnati c/o Frost Brown Todd LLC
; TITLE OF INVENTION: ADRENERGIC RECEPTOR OVEREXPRESSION IN AIRWAY TISSUES FOR THE
; TITLE OF INVENTION: TREATMENT OF AIRWAY OBSTRUCTIVE DISEASES
; FILE REFERENCE: 0091830/0483131
; CURRENT APPLICATION NUMBER: US/10/221,332A
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: PCT/US01/07522
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,404
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1242
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-221-332A-1

Query Match 100.0%; Score 19; DB 19; Length 1242;
Best Local Similarity 78.9%; Pred. No. 7.4; DB 19; Length 1242;
Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGCAGCGCTTCTTGC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 16 AACGGCAGCGCCUUCUUGC 34

RESULT 12
US-09-935-061-9
; Sequence 9, Application US/09935061
; Publication No. US20030129649A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian M.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to G protein-coupled receptors
; FILE REFERENCE: STAN213
; CURRENT APPLICATION NUMBER: US/09/935,061
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 3rd
; OTHER INFORMATION: Intracellular loop
; NAME/KEY: CDS
; LOCATION: (1)...(1251)
US-09-935-061-9

Query Match 100.0%; Score 19; DB 10; Length 1251;
Best Local Similarity 100.0%; Pred. No. 7.4; DB 10; Length 1251;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACGGCAGCGCTTCTTGC 19
| | | | | | | | | | | | | | | | | | | | | |
Db 16 AACGGCAGCGCTTCTTGC 34

RESULT 13
US-10-692-071-9
; Sequence 9, Application US/10692071
; Publication No. US20040157268A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian K.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to membrane spanning, signal-transducing proteins
; FILE REFERENCE: STAN-213CIP
; CURRENT APPLICATION NUMBER: US/10/692,071
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: PCT/US02/13250
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/935,061
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 3rd
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1251)
US-10-692-071-9

Query Match 100.0%; Score 19; DB 19; Length 1251;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGCAGCGCCTTCTTGC 19
DB 16 AACGGCAGCGCCTTCTTGC 34

RESULT 14

US-10-157-305A-15
Sequence 15, Application US/10157305A
Publication No. US20030166099A1
GENERAL INFORMATION:
APPLICANT: Sabbadini, Roger A.
APPLICANT: Surber, Mark W.
APPLICANT: Neil Berkley
APPLICANT: Anca M. Segall
APPLICANT: Robert Klepper
TITLE OF INVENTION: MINICELL COMPRISING MEMBRANE PROTEINS
FILE REFERENCE: MPEX.008DV1
CURRENT APPLICATION NUMBER: US/10/157,305A
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 60/293,566
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/359,843
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 258
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 1320
TYPE: DNA
ORGANISM: Homo sapien
US-10-157-305A-15

Query Match 100.0%; Score 19; DB 16; Length 1320;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGCAGCGCCTTCTTGC 19
DB 80 AACGGCAGCGCCTTCTTGC 98

RESULT 15

US-10-157-391-15
Sequence 15, Application US/10157391
Publication No. US20030166279A1
GENERAL INFORMATION:
APPLICANT: Sabbadini, Roger A.
APPLICANT: Neil Berkley
TITLE OF INVENTION: MINICELL-BASED TRANSFECTION
FILE REFERENCE: MPEX.008DV14
CURRENT APPLICATION NUMBER: US/10/157,391
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: 60/293,566
PRIOR FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: 60/359,843
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 10/154,951
PRIOR FILING DATE: 2002-05-24
NUMBER OF SEQ ID NOS: 257
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15

LENGTH: 1320
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion protein
US-10-157-391-15

Query Match 100.0%; Score 19; DB 16; Length 1320;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGGCAGCGCCTTCTTGC 19
DB 80 AACGGCAGCGCCTTCTTGC 98

Search completed: August 7, 2005, 15:39:58
Job time : 356.818 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 09:47:41 ; Search time 68.2273 Seconds
(without alignments)
455.672 Million cell updates/sec

Title: US-09-542-718-3

Perfect score: 19

Sequence: 1 acatgacgatgccatgcc 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents NA:*
- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
 - 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
 - 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 - 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 - 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 - 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	4 US-09-973-132-3	Sequence 3, Appli
2	19	100.0	106	4 US-09-973-132-1	Sequence 1, Appli
3	19	100.0	187	5 PCT-US91-00909-21	Sequence 21, Appli
4	19	100.0	191	5 PCT-US91-00909-20	Sequence 20, Appli
5	19	100.0	1242	5 PCT-US91-00909-3	Sequence 3, Appli
6	19	100.0	2305	4 US-09-016-434-1282	Sequence 1282, Ap
7	19	100.0	2305	4 US-09-023-653-1249	Sequence 1249, Ap
8	19	100.0	3451	4 US-09-811-286-1	Sequence 1, Appli
9	19	100.0	5857	3 US-09-293-170-4	Sequence 4, Appli
10	17.4	91.6	1942	3 US-09-313-300-3	Sequence 3, Appli
11	17	89.5	645	4 US-09-252-991A-6331	Sequence 6331, Ap
12	17	89.5	783	4 US-09-252-991A-6415	Sequence 6415, Ap
13	17	89.5	819	4 US-09-252-991A-6136	Sequence 6136, Ap
14	16.4	86.3	1257	4 US-09-489-039A-1557	Sequence 1557, Ap
15	16.4	86.3	2169	4 US-09-489-039A-1771	Sequence 1771, Ap
16	16	84.2	3935	3 US-09-060-482-1	Sequence 1, Appli
17	16	84.2	4082	4 US-09-949-016-2722	Sequence 2722, Ap
18	16	84.2	14205	4 US-09-949-016-14464	Sequence 14464, A
19	15.8	83.2	360	4 US-09-640-211A-1294	Sequence 1294, Ap
20	15.8	83.2	392	4 US-09-270-767-6358	Sequence 6358, Ap
21	15.8	83.2	392	4 US-09-270-767-6358	Sequence 6358, Ap
22	15.8	83.2	1235	4 US-09-270-767-21640	Sequence 21640, A
23	15.8	83.2	1235	4 US-09-270-767-15027	Sequence 15027, A
24	15.8	83.2	1605	4 US-09-270-767-10407	Sequence 10407, A
25	15.8	83.2	3213	4 US-09-949-016-5184	Sequence 5184, Ap
26	15.4	81.1	342	4 US-09-949-016-16926	Sequence 16926, A
27	15.4	81.1	774	4 US-09-902-540-3441	Sequence 3441, Ap
				4 US-09-602-777A-81	Sequence 81, Appli

ALIGNMENTS

RESULT 1

US-09-973-132-3

; Sequence 3, Application US/09973132

; Patent No. 6593092

; GENERAL INFORMATION:

; APPLICANT: Wu, H.

; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION

; FILE REFERENCE: 6687 US.P1

; CURRENT APPLICATION NUMBER: US/09/973,132

; CURRENT FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 09/542,718

; PRIOR FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 19

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic fragments

US-09-973-132-3

Query Match 100.0%; Score 19; DB 4; Length 19;

Best Local Similarity 100.0%; Pred.No.5.1;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATGACGATGCCCATGCC 19

Db 1 ACATGACGATGCCCATGCC 19

RESULT 2

US-09-973-132-1/c

; Sequence 1, Application US/09973132

; Patent No. 6593092

; GENERAL INFORMATION:

; APPLICANT: Wu, H.

; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION

; FILE REFERENCE: 6687 US.P1

; CURRENT APPLICATION NUMBER: US/09/973,132

; CURRENT FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 09/542,718

; PRIOR FILING DATE: 2000-04-04

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 106

; TYPE: DNA

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragment
US-09-973-132-1

Query Match          100.0%; Score 19; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 6.2; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

Qy 1 ACATGACGATGCCCATGCC 19
    |||||
Db 106 ACATGACGATGCCCATGCC 88

RESULT 3
PCT-US91-00909-21
; Sequence 21, Application PC/TUS9100909
; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej Z.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Methods of Producing Hybrid G
; TITLE OF INVENTION: Protein-Coupled Receptors
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: United States
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00909
; FILING DATE: 19910208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.408PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 191 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US91-00909-20

Query Match          100.0%; Score 19; DB 5; Length 191;
Best Local Similarity 100.0%; Pred. No. 6.7; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

Qy 1 ACATGACGATGCCCATGCC 19
    |||||
Db 176 ACATGACGATGCCCATGCC 158

RESULT 5
PCT-US91-00909-3/c
; Sequence 3, Application PC/TUS9100909
; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej Z.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Methods of Producing Hybrid G
; TITLE OF INVENTION: Protein-Coupled Receptors
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: United States
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00909
; FILING DATE: 19910208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.408PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 187 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US91-00909-21

Query Match          100.0%; Score 19; DB 5; Length 187;
Best Local Similarity 100.0%; Pred. No. 6.7; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

Qy 1 ACATGACGATGCCCATGCC 19
    |||||
Db 16 ACATGACGATGCCCATGCC 34

RESULT 4
PCT-US91-00909-20/c
; Sequence 20, Application PC/TUS9100909
; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej Z.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Methods of Producing Hybrid G
; TITLE OF INVENTION: Protein-Coupled Receptors
```

```

; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1242 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1242
PCT-US91-00909-3

Query Match 100.0%; Score 19; DB 5; Length 1242;
Best Local Similarity 100.0%; Pred. No. 8.3; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY 1 ACATGACGATGCCCATGCC 19
Db 121 ACATGACGATGCCCATGCC 103

RESULT 6
US-09-016-434-1282/c
; Sequence 1282, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1282:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 929370
US-09-016-434-1282

Query Match 100.0%; Score 19; DB 4; Length 2305;
Best Local Similarity 100.0%; Pred. No. 8.3; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY 1 ACATGACGATGCCCATGCC 19
Db 121 ACATGACGATGCCCATGCC 103

RESULT 7
US-09-023-655-1249/c
; Sequence 1249, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1249:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2305 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 929370
US-09-023-655-1249

Query Match 100.0%; Score 19; DB 4; Length 2305;
Best Local Similarity 100.0%; Pred. No. 8.9; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY 1 ACATGACGATGCCCATGCC 19
Db 914 ACATGACGATGCCCATGCC 896

RESULT 8
US-09-811-286-1/c
; Sequence 1, Application US/09811286
; Patent No. 6586183
; GENERAL INFORMATION:
; APPLICANT: Drysdale, Connie M
; APPLICANT: Judson, Richard S
```

```
; APPLICANT: Liggett, Stephen B
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stack, Catherine B.
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: Association of beta2-adrenergic receptor haplotypes
; TITLE OF INVENTION: with drug response
; FILE REFERENCE: MWH-0303U81
; CURRENT APPLICATION NUMBER: US/09/811,286
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3451
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1588)..(2829)
US-09-811-286-1

Query Match      100.0%; Score 19; DB 4; Length 3451;
Best Local Similarity 100.0%; Pred. No. 9.4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATGACGATGCCCATGCC 19
Db 1708 ACATGACGATGCCCATGCC 1690

RESULT 9
US-09-293-170-4/c
; Sequence 4, Application US/09293170
; Patent No. 6383777
; GENERAL INFORMATION:
; APPLICANT: Brever, Richard M.
; APPLICANT: Ma, Lijun
; APPLICANT: Kennedy, Chris
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH YIELD
; TITLE OF INVENTION: PRODUCTION OF EUKARYOTIC PROTEINS
; FILE REFERENCE: 22000.0094
; CURRENT APPLICATION NUMBER: US/09/293,170
; CURRENT FILING DATE: 1999-04-16
; EARLIER APPLICATION NUMBER: 60/081,989
; EARLIER FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 5857
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (300)...(1799)
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: Synthetic construct
US-09-293-170-4

Query Match      100.0%; Score 19; DB 3; Length 5857;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATGACGATGCCCATGCC 19
Db 654 ACATGACGATGCCCATGCC 636

RESULT 10
US-09-313-300-3
; Sequence 3, Application US/09313300
; Patent No. 622027
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew, R.
; APPLICANT: Lal, Preeti
```

```
; APPLICANT: Yue, Henry
; APPLICANT: Tang, Tom, Y.
; APPLICANT: Baughn, Mariah, R.
; APPLICANT: Azinzai, Valda
; TITLE OF INVENTION: MOLECULES EXPRESSED IN HIPPOCAMPUS
; FILE REFERENCE: PB-0012 US
; CURRENT APPLICATION NUMBER: US/09/313,300
; CURRENT FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 1942
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 357, 514, 515, 545, 547, (554)...(582)
; OTHER INFORMATION: a or g or c or t, unknown, or other
; FEATURE:
; NAME/KEY:
; OTHER INFORMATION: 244771
; PUBLICATION INFORMATION:
US-09-313-300-3

Query Match      91.6%; Score 17.4; DB 3; Length 1942;
Best Local Similarity 94.7%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ACATGACGATGCCCATGCC 19
Db 605 ACATGACGATGCCCATGCC 623

RESULT 11
US-09-252-991A-6331/c
; Sequence 6331, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6331
; LENGTH: 645
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6331

Query Match      89.5%; Score 17; DB 4; Length 645;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ATGACGATGCCCATGCC 19
Db 216 ATGACGATGCCCATGCC 200

RESULT 12
US-09-252-991A-6415/c
; Sequence 6415, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
```


TYPE: DNA
ORGANISM: *Klebsiella pneumoniae*
US-09-489-039A-1557

Search completed: August 7, 2005, 11:52:18
Job time : 73.2273 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 11:37:03 ; Search time 355.818 Seconds
(without alignments)
346.144 Million cell updates/sec

Title: US-09-542-718-3

Perfect score:

Sequence: 1 acatgacgatgcccatgcc 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 200000000
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:**

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	19	100.0	19	9	US-09-973-132-3	Sequence 3, Appli
C 2	19	100.0	106	9	US-09-973-132-1	Sequence 1, Appli
C 3	19	100.0	521	16	US-10-029-386-9056	Sequence 9056, Ap
C 4	19	100.0	1021	17	US-10-321-039-28	Sequence 28, Appl
C 5	19	100.0	1021	17	US-10-321-039-29	Sequence 29, Appl
C 6	19	100.0	1113	9	US-09-993-844-9	Sequence 9, Appli
C 7	19	100.0	1113	23	US-11-026-435-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-09-973-132-3

; Sequence 3, Application US/09973132

; Patent No. US20020137069A1

; GENERAL INFORMATION:

APPLICANT: WU, H.

APPLICANT: Merchant, B.T.

10 TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION

FILE REFERENCE: 6687.US.P1

; CURRENT APPLICATION NUMBER: US/09/973,132

;; CURRENT FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: 09/542,718

; PRIOR FILING DATE: 2000-04

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 1

```
; TYPE: DNA
```

; ORGANISM: Artificial Sequence

; FEATURE:

OTHER INFORMATION: synthetic fragments

US-09-973-132-3

Query Match	100.0%; Score 19; DB 9; Length 19;
-------------	------------------------------------

QY 1 ACATGACGATGCCCATGCC 19

100

```
RESULT 2
US-09-973-132-1/c
; Sequence 1, Application US/09973132
; Patent No. US20020137069A1
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; APPLICANT: Merchant, B.T.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687.US.P1
; CURRENT APPLICATION NUMBER: US/09/973,132
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 2001-10-09
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 106
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragment
US-09-973-132-1
Query Match 100.0%; Score 19; DB 9; Length 106;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATGACGATGCCCATGCC 19
Db 106 ACATGACGATGCCCATGCC 88

RESULT 3
US-10-029-386-9056/c
; Sequence 9056, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 9056
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC011334.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: SWISSPROT HIT: P07550, EVALUATE 5.00e-99
; OTHER INFORMATION: NT HIT: AF022954.1, EVALUATE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AL553611.1, EVALUATE 0.00e+00
US-10-029-386-9056
Query Match 100.0%; Score 19; DB 16; Length 521;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATGACGATGCCCATGCC 19
Db 36 ACATGACGATGCCCATGCC 18
```

```
RESULT 4
US-10-321-039-28/c
; Sequence 28, Application US/10321039
; Publication No. US20040014067A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kurensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: {561}..(561)
; OTHER INFORMATION: n can be a or g.
US-10-321-039-28
Query Match 100.0%; Score 19; DB 17; Length 1021;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACATGACGATGCCCATGCC 19
Db 636 ACATGACGATGCCCATGCC 618

RESULT 5
US-10-321-039-29/c
; Sequence 29, Application US/10321039
; Publication No. US20040014067A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kurensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: {561}..(561)
; OTHER INFORMATION: n can be c or t.
US-10-321-039-29
Query Match 100.0%; Score 19; DB 17; Length 1021;
Best Local Similarity 100.0%; Pred. No. 14;
```

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATGACGATGCCCATGCC 19
|||||
Db 191 ACATGACGATGCCCATGCC 173

RESULT 6

US-09-993-844-9/c
; Sequence 9, Application US/09993844
; Patent No. US20020106739A1
; GENERAL INFORMATION:
; APPLICANT: Oakley, Robert H.
; APPLICANT: Barak, Lawrence S.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Modified G-Protein Coupled Receptors
; FILE REFERENCE: 033072-026
; CURRENT APPLICATION NUMBER: US/09/993,844
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,772
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/260,363
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of beta2AR-V2R chimera
US-09-993-844-9

Query Match 100.0%; Score 19; DB 9; Length 1113;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATGACGATGCCCATGCC 19
|||||
Db 121 ACATGACGATGCCCATGCC 103

RESULT 7

US-11-026-435-9/c
; Sequence 9, Application US/11026435
; Publication No. US20050106623A1
; GENERAL INFORMATION:
; APPLICANT: Oakley, Robert H.
; APPLICANT: Barak, Lawrence S.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Modified G-Protein Coupled Receptors
; FILE REFERENCE: 033072-026
; CURRENT APPLICATION NUMBER: US/11/026,435
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: US/09/993,844
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,772
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/260,363
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of beta2AR-V2R chimera
US-11-026-435-9

Query Match 100.0%; Score 19; DB 23; Length 1113;

Best Local Similarity 100.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATGACGATGCCCATGCC 19
|||||
Db 121 ACATGACGATGCCCATGCC 103

RESULT 8

US-09-935-061-5/c
; Sequence 5, Application US/09935061
; Publication No. US20030129649A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian M.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; FILE REFERENCE: STAN213
; CURRENT APPLICATION NUMBER: US/09/935,061
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-09-935-061-5

Query Match 100.0%; Score 19; DB 10; Length 1239;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATGACGATGCCCATGCC 19
|||||
Db 121 ACATGACGATGCCCATGCC 103

RESULT 9

US-09-935-061-7/c
; Sequence 7, Application US/09935061
; Publication No. US20030129649A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian M.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; FILE REFERENCE: STAN213
; CURRENT APPLICATION NUMBER: US/09/935,061
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 2nd
; OTHER INFORMATION: Intracellular loop
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-09-935-061-7

Query Match 100.0%; Score 19; DB 10; Length 1239;

```
; OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 2nd
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-10-692-071-7

Query Match 100.0%; Score 19; DB 19; Length 1239;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATGACGATGCCCATGCC 19
   |||||
Db 121 ACATGACGATGCCCATGCC 103

RESULT 10
US-10-692-071-5/c
; Sequence 5, Application US/10692071
; Publication No. US20040157268A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian K.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to membrane spanning, signal-transducing proteins
; FILE REFERENCE: STAN-213CIP
; CURRENT APPLICATION NUMBER: US/10/692,071
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: PCT/US02/13250
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/935,061
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-10-692-071-5

Query Match 100.0%; Score 19; DB 19; Length 1239;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATGACGATGCCCATGCC 19
   |||||
Db 121 ACATGACGATGCCCATGCC 103

RESULT 11
US-10-692-071-7/c
; Sequence 7, Application US/10692071
; Publication No. US20040157268A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian K.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to membrane spanning, signal-transducing proteins
; FILE REFERENCE: STAN-213CIP
; CURRENT APPLICATION NUMBER: US/10/692,071
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: PCT/US02/13250
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/935,061
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 3rd
; OTHER INFORMATION: Intracellular loop

; OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 2nd
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-10-692-071-7

Query Match 100.0%; Score 19; DB 19; Length 1239;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATGACGATGCCCATGCC 19
   |||||
Db 121 ACATGACGATGCCCATGCC 103

RESULT 12
US-10-221-332A-1/c
; Sequence 1, Application US/10221332A
; Publication No. US20040192625A1
; GENERAL INFORMATION:
; APPLICANT: University of Cincinnati c/o Frost Brown Todd LLC
; TITLE OF INVENTION: ADRENERGIC RECEPTOR OVEREXPRESSION IN AIRWAY TISSUES FOR THE
; TITLE OF INVENTION: TREATMENT OF AIRWAY OBSTRUCTIVE DISEASES
; FILE REFERENCE: 0091830/0483131
; CURRENT APPLICATION NUMBER: US/10/221,332A
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: PCT/US01/07522
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,404
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1
; LENGTH: 1242
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-10-221-332A-1

Query Match 100.0%; Score 19; DB 19; Length 1242;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACATGACGATGCCCATGCC 19
   |||||
Db 121 ACATGACGATGCCCATGCC 103

RESULT 13
US-09-935-061-9/c
; Sequence 9, Application US/09935061
; Publication No. US20030129649A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian M.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to G protein-coupled receptors
; FILE REFERENCE: STAN213
; CURRENT APPLICATION NUMBER: US/09/935,061
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 3rd
; OTHER INFORMATION: Intracellular loop
```

```
; NAME/KEY: CDS
; LOCATION: (1)... (1251)
US-09-935-061-9

Query Match      100.0%; Score 19; DB 10; Length 1251;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ACATGACGATGCCCATGCC 19
Db      121 ACATGACGATGCCCATGCC 103

RESULT 14
US-10-692-071-9/c
; Sequence 9, Application US/10692071
; Publication No. US20040157268A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian K.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to membrane spanning, signal-transducing proteins
; FILE REFERENCE: STAN-213CIP
; CURRENT APPLICATION NUMBER: US/10/692,071
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: PCT/US02/13250
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/935,061
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 3rd
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)... (1251)
US-10-692-071-9

Query Match      100.0%; Score 19; DB 19; Length 1251;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ACATGACGATGCCCATGCC 19
Db      121 ACATGACGATGCCCATGCC 103

RESULT 15
US-10-157-305A-15/c
; Sequence 15, Application US/10157305A
; Publication No. US20030166099A1
; GENERAL INFORMATION:
; APPLICANT: Sabbadini, Roger A.
; APPLICANT: Surber, Mark W.
; APPLICANT: Neil Berkley
; APPLICANT: Anca M. Segall
; APPLICANT: Robert Klepper
; TITLE OF INVENTION: MINICELL COMPRISING MEMBRANE PROTEINS
; FILE REFERENCE: MPEX.008DV1
; CURRENT APPLICATION NUMBER: US/10/157,305A
; CURRENT FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: 60/293,566
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/359,843
; PRIOR FILING DATE: 2002-02-25

; PRIOR APPLICATION NUMBER: 10/154,951
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 258
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 1320
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-157-305A-15

Query Match      100.0%; Score 19; DB 16; Length 1320;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ACATGACGATGCCCATGCC 19
Db      185 ACATGACGATGCCCATGCC 167

Search completed: August 7, 2005, 15:39:58
Job time : 355.818 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 09:47:41 ; Search time 53.8636 Seconds
(without alignments)
455.672 Million cell updates/sec

Title: US-09-542-718-4
Perfect score: 15
Sequence: 1 caatagaagccatgc 15

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	US-09-973-132-4	Sequence 4, Appli
2	15	100.0	54	US-09-336-228B-1	Sequence 1, Appli
3	15	100.0	60	US-09-336-228B-2	Sequence 2, Appli
4	15	100.0	106	US-09-973-132-1	Sequence 1, Appli
5	15	100.0	1242	PCT-US91-00909-3	Sequence 3, Appli
6	15	100.0	2305	US-09-016-434-1282	Sequence 1282, Ap
7	15	100.0	2305	US-09-023-655-1249	Sequence 1249, Ap
8	15	100.0	3451	US-09-811-286-1	Sequence 1, Appli
9	14.6	97.3	21	US-09-657-472-1254	Sequence 1254, Ap
10	14	93.3	21	US-09-009-443-21	Sequence 21, Appli
11	14	93.3	601	US-09-949-016-168873	Sequence 168873, Ap
12	14	93.3	1086	US-09-328-352-2232	Sequence 2232, Ap
13	14	93.3	2121	US-08-633-879C-17	Sequence 17, Appli
14	14	93.3	2214	US-09-543-681A-2317	Sequence 2317, Ap
15	14	93.3	3684	US-09-688-188B-104	Sequence 104, App
16	14	93.3	3684	US-09-291-417D-104	Sequence 104, App
17	14	93.3	35803	US-09-949-016-11863	Sequence 11863, A
18	14	93.3	35804	US-09-949-016-12962	Sequence 12962, A
19	14	93.3	38261	US-09-949-016-13802	Sequence 13802, A
20	14	93.3	51620	US-09-949-016-12848	Sequence 12848, A
21	14	93.3	51621	US-09-949-016-16503	Sequence 16503, A
22	14	93.3	98844	US-09-791-211-10	Sequence 10, Appli
23	14	93.3	143776	US-09-949-001-29	Sequence 29, Appli
24	14	93.3	144034	US-09-949-001-35	Sequence 35, Appli
25	13.4	89.3	197	US-09-640-211A-13	Sequence 13, Appli
26	13.4	89.3	565	US-09-270-767-9689	Sequence 9689, Ap
27	13.4	89.3	565	US-09-270-767-24971	Sequence 24971, A

ALIGNMENTS

RESULT 1

US-09-973-132-4
; Sequence 4, Application US/09973132
; Patent No. 6593092
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; APPLICANT: Merchant, B.T.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687 US.P1
; CURRENT APPLICATION NUMBER: US/09/973,132
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragments
US-09-973-132-4

Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATGC 15
| | | | | | | | | | | | | | | | | |
Db 1 CAATAGAAGCCATGC 15

RESULT 2

US-09-336-228B-1/c
; Sequence 1, Application US/09336228B
; Patent No. 6214187
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Boles, T. Christian
; TITLE OF INVENTION: Denaturing Gradient Affinity
; FILE REFERENCE: MST98-02pa
; CURRENT APPLICATION NUMBER: US/09/336,228B
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/089,788
; PRIOR FILING DATE: 1998-06-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 54

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-336-228B-1

Query Match 100.0%; Score 15; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATGC 15
| | | | | | | | | | | | | | |
Db 48 CAATAGAAGCCATGC 34

RESULT 3
US-09-336-228B-2/c
; Sequence 2, Application US/09336228B
; Patent No. 6214187
; GENERAL INFORMATION:
; APPLICANT: Hammond, Philip W.
; APPLICANT: Boles, T. Christian
; TITLE OF INVENTION: Denaturing Gradient Affinity
; FILE REFERENCE: M8798-02pA
; CURRENT APPLICATION NUMBER: US/09/336,228B
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/089,788
; PRIOR FILING DATE: 1998-06-18
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-336-228B-2

Query Match 100.0%; Score 15; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 66;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATGC 15
| | | | | | | | | | | | | | |
Db 48 CAATAGAAGCCATGC 34

RESULT 4
US-09-973-132-1
; Sequence 1, Application US/09973132
; Patent No. 6593092
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; APPLICANT: Merchant, B.T.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687.US.P1
; CURRENT APPLICATION NUMBER: US/09/973,132
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 106
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragment
US-09-973-132-1

Query Match 100.0%; Score 15; DB 4; Length 106;
Best Local Similarity 100.0%; Pred. No. 71;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CAATAGAAGCCATGC 15
| | | | | | | | | | | | | | |
Db 27 CAATAGAAGCCATGC 41

RESULT 5
PCT-US91-00909-3
; Sequence 3, Application PC/TUS9100909
; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej Z.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: Methods of Producing Hybrid G
; TITLE OF INVENTION: Protein-Coupled Receptors
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Ave.
; CITY: Seattle
; STATE: Washington
; COUNTRY: United States
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/00909
; FILING DATE: 19910208
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 990008.408PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; TELEFAX: 206-682-6031
; TELEX: 3723836
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1242 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1242
PCT-US91-00909-3

Query Match 100.0%; Score 15; DB 5; Length 1242;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATGC 15
| | | | | | | | | | | | | | |
Db 42 CAATAGAAGCCATGC 56

RESULT 6
US-09-016-434-1282
; Sequence 1282, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Sellhauer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1282:
SEQUENCE CHARACTERISTICS:
LENGTH: 2305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 929370
US-09-016-434-1282

Query Match 100.0%; Score 15; DB 4; Length 2305;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATAGAGCCATGC 15
Db 835 CAATAGAGCCATGC 849

RESULT 7
US-09-023-655-1249
Sequence 1249, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1249:
SEQUENCE CHARACTERISTICS:
LENGTH: 2305 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: 929370
US-09-023-655-1249

Query Match 100.0%; Score 15; DB 4; Length 2305;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATAGAGCCATGC 15
Db 835 CAATAGAGCCATGC 849

RESULT 8
US-09-811-286-1
Sequence 1, Application US/09811286
Patent No. 6586183
GENERAL INFORMATION:
APPLICANT: Drysdale, Connie M
APPLICANT: Judson, Richard S
APPLICANT: Liggett, Stephen B
APPLICANT: Mandabalan, Krishnan
APPLICANT: Stack, Catherine B.
APPLICANT: Stephens, J. Claiborne
TITLE OF INVENTION: Association of beta2-adrenergic receptor haplotypes
TITLE OF INVENTION: with drug response
FILE REFERENCE: MWH-0303US1
CURRENT APPLICATION NUMBER: US/09/811,286
CURRENT FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 1
LENGTH: 3451
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1588)..(2829)
US-09-811-286-1

Query Match 100.0%; Score 15; DB 4; Length 3451;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATAGAGCCATGC 15
Db 1629 CAATAGAGCCATGC 1643

RESULT 9
US-09-657-472-1254
Sequence 1254, Application US/09657472
Patent No. 6727063
GENERAL INFORMATION:
APPLICANT: Lander, Eric S.
APPLICANT: Cargill, Michele

; APPLICANT: Ireland, James S.
; APPLICANT: Bolk, Stacey
; APPLICANT: Daley, George Q.
; APPLICANT: McCarthy, Jeanette J.
; TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
; FILE REFERENCE: 2825-1027-001
; CURRENT APPLICATION NUMBER: US/09/657,472
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: US 60/153,357
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 60/220,947
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: US 60/225,724
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2551
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1254
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-657-472-1254

Query Match 97.3%; Score 14.6; DB 4; Length 21;
Best Local Similarity 93.3%; Pred. No. 98;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATGC 15
Db 7 CAATAGAAGCCATGC 21

RESULT 10
US-09-009-443-21
; Sequence 21, Application US/09009443
; Patent No. 6259003
; GENERAL INFORMATION:
; APPLICANT: Fujisawa, Koichi
; APPLICANT: Kasukabe, Yoshihisa
; APPLICANT: Nishiguchi, Susumu
; APPLICANT: Maekawa, Yoshihiko
; APPLICANT: Allen, Randy Dale
; TITLE OF INVENTION: PLANT PROMOTERS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 2000 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/009,443
; FILING DATE: 20-JAN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Mays, Thomas D.
; REGISTRATION NUMBER: 34,524
; REFERENCE/DOCKET NUMBER: 20455-20113.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/887-1500
; TELEFAX: 202/887-0763
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid synthetic DNA
US-09-009-443-21

Query Match 93.3%; Score 14; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATG 14
Db 2 CAATAGAAGCCATG 15

RESULT 11

US-09-949-016-168873
; Sequence 168873, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 168873
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-168873

Query Match 93.3%; Score 14; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATG 14
Db 384 CAATAGAAGCCATG 397

RESULT 12

US-09-328-352-2232/c
; Sequence 2232, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 2232
; LENGTH: 1086
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2232

Query Match 93.3%; Score 14; DB 4; Length 1086;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATG 14
Db 712 CAATAGAAGCCATG 699

RESULT 13

US-08-633-879C-17

Sequence 17, Application US/08633879C
Patent No. 5928922
GENERAL INFORMATION:
APPLICANT: Kivirikko, Kari I.
APPLICANT: Pihlajaniemi, Taina
APPLICANT: Helakoski, Tarja I.
APPLICANT: Annunen, Pia P.
APPLICANT: Nissi, Ritva K.
APPLICANT: No. 5928922elainen, Minna K.
TITLE OF INVENTION: '2 SUBUNIT OF PROLYL-4-HYDROXYLASE
NUCLEIC ACID SEQUENCES ENCODING SUCH SUBUNIT AND
METHODS FOR PRODUCING THE SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/633,879C
FILING DATE: 10-APR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
REFERENCE/DOCKET NUMBER: 8389-0041-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2121 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 96...272
OTHER INFORMATION:
US-08-633-879C-17

Query Match 93.3%; Score 14; DB 2; Length 2121;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AATAGAAGCCATGC 15
|||||
Db 1880 AATAGAAGCCATGC 1893

RESULT 14
US-09-543-681A-2317/c
Sequence 2317, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2317
LENGTH: 2214
TYPE: DNA
ORGANISM: Proteus mirabilis
US-09-543-681A-2317

Query Match 93.3%; Score 14; DB 4; Length 2214;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATG 14
|||||
Db 1870 CAATAGAAGCCATG 1857

RESULT 15
US-09-688-188B-104
Sequence 104, Application US/09688188B
Patent No. 6656716
GENERAL INFORMATION:
APPLICANT: FLOWMAN, GREGORY
APPLICANT: MARTINEZ, RICARDO
APPLICANT: WHYTE, DAVID
TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
FILE REFERENCE: 038602/0328
CURRENT APPLICATION NUMBER: US/09/688,188B
CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 09/291,417
PRIOR FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 60/081,784
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 104
TYPE: DNA
LENGTH: 3684
ORGANISM: Homo sapiens
US-09-688-188B-104

Query Match 93.3%; Score 14; DB 4; Length 3684;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATG 14
|||||
Db 2151 CAATAGAAGCCATG 2164

Search completed: August 7, 2005, 11:52:20
Job time : 55.8636 secs

This Page Blank (used)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 11:37:03 ; Search time 280.909 Seconds
(without alignments)
346.144 Million cell updates/sec

Title: US-09-542-718-4

Perfect score: 15

Sequence: 1 caatagaagccatgc 15

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	15	9	US-09-973-132-4
2	15	100.0	106	9	US-09-973-132-1
3	15	100.0	198	19	US-10-437-963-96348
4	15	100.0	654	13	US-10-027-632-30178
5	15	100.0	654	17	US-10-027-632-30178
6	15	100.0	1021	17	US-10-321-039-29
7	15	100.0	1113	9	US-09-993-844-9

8	15	100.0	1113	23	US-11-026-435-9	Sequence 9, Appli
9	15	100.0	1217	19	US-10-767-701-12459	Sequence 12459, A
10	15	100.0	1239	10	US-09-935-061-5	Sequence 5, Appli
11	15	100.0	1239	10	US-09-935-061-7	Sequence 7, Appli
12	15	100.0	1239	19	US-10-692-071-5	Sequence 5, Appli
13	15	100.0	1239	19	US-10-692-071-7	Sequence 7, Appli
14	15	100.0	1242	19	US-10-221-332A-1	Sequence 1, Appli
15	15	100.0	1251	10	US-09-935-061-9	Sequence 9, Appli
16	15	100.0	1251	19	US-10-692-071-9	Sequence 9, Appli
17	15	100.0	1362	19	US-10-437-963-73340	Sequence 73340, A
18	15	100.0	1369	14	US-10-116-802-111	Sequence 111, App
19	15	100.0	2015	15	US-10-225-567A-51	Sequence 51, Appl
20	15	100.0	2015	21	US-10-888-313A-1	Sequence 1, Appli
21	15	100.0	2054	10	US-09-814-353-20018	Sequence 20018, A
22	15	100.0	2305	15	US-10-309-515-23	Sequence 23, Appl
23	15	100.0	2305	15	US-10-101-510-181	Sequence 181, App
24	15	100.0	2305	16	US-10-126-764-23	Sequence 23, Appl
25	15	100.0	2305	17	US-10-305-720-1282	Sequence 1282, Ap
26	15	100.0	2305	18	US-10-641-643-1249	Sequence 1249, Ap
27	15	100.0	2502	18	US-10-425-114-25016	Sequence 25016, A
28	15	100.0	2815	17	US-10-374-780A-548	Sequence 548, App
29	15	100.0	2815	18	US-10-412-699B-1041	Sequence 1041, Ap
30	15	100.0	2864	20	US-10-425-115-11525	Sequence 11525, A
31	15	100.0	2924	20	US-10-425-115-11590	Sequence 11590, A
32	15	100.0	3451	9	US-09-811-286-1	Sequence 1, Appli
33	15	100.0	3451	9	US-09-954-456-214	Sequence 214, App
34	15	100.0	3451	9	US-09-954-456-1598	Sequence 1598, Ap
35	15	100.0	3451	9	US-09-990-596-2	Sequence 2, Appli
36	15	100.0	3451	10	US-09-811-285-1	Sequence 1, Appli
37	15	100.0	3451	21	US-10-843-641A-3241	Sequence 3241, Ap
38	15	100.0	3451	21	US-10-843-641A-4625	Sequence 4625, Ap
39	15	100.0	3659	13	US-10-044-090-27	Sequence 27, Appl
40	15	100.0	3659	15	US-10-101-510-411	Sequence 411, App
41	15	100.0	4473	20	US-10-425-115-18848	Sequence 18848, A
42	15	100.0	6062	16	US-10-353-908-6	Sequence 6, Appli
43	14	93.3	25	22	US-10-719-956-421353	Sequence 421353,
44	14	93.3	201	19	US-10-741-601-6998	Sequence 6998, Ap
45	14	93.3	201	21	US-10-741-600-19495	Sequence 19495, A

ALIGNMENTS

RESULT 1
US-09-973-132-4
; Sequence 4, Application US/09973132
; Patent No. US20020137069A1
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; APPLICANT: Merchant, B.T.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687.US.PI
; CURRENT APPLICATION NUMBER: US/09/973,132
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragments
US-09-973-132-4

Query Match	100.0%	Score 15;	DB 9;	Length 15;
Best Local Similarity	100.0%	Pred. No. 1.7e+02;		
Matches	15;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Qy	1	CAATAGAAGCCATGC	15	
Db	1	CAATAGAAGCCATGC	15	

```
RESULT 2
US-09-973-132-1
; Sequence 1, Application US/09973132
; Patent No. US20020137069A1
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; APPLICANT: Merchant, B.T.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687.US.P1
; CURRENT APPLICATION NUMBER: US/09/973,132
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 106
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragment
US-09-973-132-1

Query Match          100.0%; Score 15; DB 9; Length 106;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAATAGAGCCATGC 15
Db      27 CAATAGAGCCATGC 41

RESULT 3
US-10-437-963-96348/c
; Sequence 96348, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 96348
; LENGTH: 198
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_94452C.1
US-10-437-963-96348

Query Match          100.0%; Score 15; DB 19; Length 198;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAATAGAGCCATGC 15
Db      154 CAATAGAGCCATGC 140

RESULT 4
US-10-027-632-30178
; Sequence 30178, Application US/10027632
```

```
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30178
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-30178

Query Match          100.0%; Score 15; DB 13; Length 654;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CAATAGAGCCATGC 15
Db      473 CAATAGAGCCATGC 487

RESULT 5
US-10-027-632-30178
; Sequence 30178, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30178
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-30178

Query Match          100.0%; Score 15; DB 17; Length 654;
```


Best Local Similarity 100.0%; Pred. No. 2.5e+02; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATAGAAGCCATGC 15
|||||
Db 473 CAATAGAAGCCATGC 487

RESULT 6

US-10-321-039-29
; Sequence 29, Application US/10321039
; Publication No. US20040014067A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichiev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kurensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 1021
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (561)..(561)
; OTHER INFORMATION: n can be c or t.
US-10-321-039-29

Query Match 100.0%; Score 15; DB 17; Length 1021;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATAGAAGCCATGC 15
|||||
Db 112 CAATAGAAGCCATGC 126

RESULT 7

US-09-993-844-9
; Sequence 9, Application US/09953844
; Patent No. US20020106739A1
; GENERAL INFORMATION:
; APPLICANT: Oakley, Robert H.
; APPLICANT: Barak, Lawrence S.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Modified G-Protein Coupled Receptors
; FILE REFERENCE: 033072-026
; CURRENT APPLICATION NUMBER: US/09/993,844
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,772
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/260,363
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of beta2AR-V2R chimera

US-09-993-844-9

Query Match 100.0%; Score 15; DB 9; Length 1113;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATAGAAGCCATGC 15
|||||
Db 42 CAATAGAAGCCATGC 56

RESULT 8

US-11-026-435-9
; Sequence 9, Application US/11026435
; Publication No. US20050106623A1
; GENERAL INFORMATION:
; APPLICANT: Oakley, Robert H.
; APPLICANT: Barak, Lawrence S.
; APPLICANT: Laporte, Stephane A.
; APPLICANT: Caron, Marc G.
; TITLE OF INVENTION: Modified G-Protein Coupled Receptors
; FILE REFERENCE: 033072-026
; CURRENT APPLICATION NUMBER: US/11/026,435
; CURRENT FILING DATE: 2004-12-30
; PRIOR APPLICATION NUMBER: US/09/993,844
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: US 60/245,772
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: US 60/260,363
; PRIOR FILING DATE: 2001-01-08
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotide sequence of beta2AR-V2R chimera
US-11-026-435-9

Query Match 100.0%; Score 15; DB 23; Length 1113;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATAGAAGCCATGC 15
|||||
Db 42 CAATAGAAGCCATGC 56

RESULT 9

US-10-767-701-12459/c
; Sequence 12459, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 12459
; LENGTH: 1217
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS1301_1
US-10-767-701-12459

Query Match 100.0%; Score 15; DB 19; Length 1217;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATGC 15
|||||
Db 51 CAATAGAAGCCATGC 37

RESULT 10
US-09-935-061-5
; Sequence 5, Application US/09935061
; Publication No. US20030129649A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian M.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to G protein-coupled receptors
; FILE REFERENCE: STAN213
; CURRENT APPLICATION NUMBER: US/09/935,061
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-09-935-061-5

Query Match 100.0%; Score 15; DB 10; Length 1239;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATGC 15
|||||
Db 42 CAATAGAAGCCATGC 56

RESULT 11
US-09-935-061-7
; Sequence 7, Application US/09935061
; Publication No. US20030129649A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian M.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to G protein-coupled receptors
; FILE REFERENCE: STAN213
; CURRENT APPLICATION NUMBER: US/09/935,061
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 2nd
; OTHER INFORMATION: intracellular loop
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-09-935-061-7

Query Match 100.0%; Score 15; DB 10; Length 1239;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATGC 15
|||||
Db 42 CAATAGAAGCCATGC 56

RESULT 12
US-10-692-071-5
; Sequence 5, Application US/10692071
; Publication No. US20040157268A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian K.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to membrane spanning, signal-transducing proteins
; FILE REFERENCE: STAN-213CIP
; CURRENT APPLICATION NUMBER: US/10/692,071
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: PCT/US02/13250
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/935,061
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-10-692-071-5

Query Match 100.0%; Score 15; DB 19; Length 1239;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAATAGAAGCCATGC 15
|||||
Db 42 CAATAGAAGCCATGC 56

RESULT 13
US-10-692-071-7
; Sequence 7, Application US/10692071
; Publication No. US20040157268A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian K.
; APPLICANT: Ghanouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to membrane spanning, signal-transducing proteins
; FILE REFERENCE: STAN-213CIP
; CURRENT APPLICATION NUMBER: US/10/692,071
; CURRENT FILING DATE: 2003-10-22
; PRIOR APPLICATION NUMBER: PCT/US02/13250
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 09/935,061
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 2nd

```

; OTHER INFORMATION: intracellular loop
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1239)
US-10-692-071-7
Query Match 100.0%; Score 15; DB 19; Length 1239;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATAGAGCCATGC 15
Db 42 CAATAGAGCCATGC 56

RESULT 14
US-10-221-332A-1
; Sequence 1, Application US/10221332A
; Publication No. US20040192625A1
; GENERAL INFORMATION:
; APPLICANT: University of Cincinnati c/o Frost Brown Todd LLC
; TITLE OF INVENTION: ADRENERGIC RECEPTOR OVEREXPRESSION IN AIRWAY TISSUES FOR THE
; TREATMENT OF AIRWAY OBSTRUCTIVE DISEASES
; FILE REFERENCE: 0091830/0483131
; CURRENT APPLICATION NUMBER: US/10/221,332A
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: PCT/US01/07522
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,404
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1242
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-221-332A-1
Query Match 100.0%; Score 15; DB 19; Length 1242;
Best Local Similarity 86.7%; Pred. No. 2.6e+02;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATAGAGCCATGC 15
Db 42 CAATAGAGCCATGC 56

RESULT 15
US-09-935-061-9
; Sequence 9, Application US/09935061
; Publication No. US20030129649A1
; GENERAL INFORMATION:
; APPLICANT: Kobilka, Brian M.
; APPLICANT: Ghannouni, Pejman
; APPLICANT: Lee, Tae Weon
; TITLE OF INVENTION: Conformational assays to detect binding
; TITLE OF INVENTION: to G protein-coupled receptors
; FILE REFERENCE: STAN213
; CURRENT APPLICATION NUMBER: US/09/935,061
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Beta-2 Adrenergic Receptor with TEV site in 3rd
; OTHER INFORMATION: intracellular loop
; NAME/KEY: CDS

```

```

; LOCATION: (1)...(1251)
US-09-935-061-9
Query Match 100.0%; Score 15; DB 10; Length 1251;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAATAGAGCCATGC 15
Db 42 CAATAGAGCCATGC 56

Search completed: August 7, 2005, 15:39:59
Job time : 281.909 secs

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 09:47:41 ; Search time 46.6818 Seconds
(without alignments)
455.672 Million cell updates/sec

Title: US-09-542-718-5
Perfect score: 13
Sequence: 1 cccaatggaagcc 13

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	13	4	US-09-973-132-5
2	13	100.0	29	4	US-09-973-132-8
3	13	100.0	29	4	US-09-973-132-9
4	13	100.0	425	4	US-09-621-976-14538
5	13	100.0	601	4	US-09-949-016-18501
6	13	100.0	601	4	US-09-949-016-18501
7	13	100.0	601	4	US-09-949-016-18501
8	13	100.0	601	4	US-09-949-016-18501
9	13	100.0	601	4	US-09-949-016-18501
10	13	100.0	1014	4	US-09-902-540-3385
11	13	100.0	4446	4	US-09-214-916A-1
12	13	100.0	5857	3	US-09-293-170-4
13	13	100.0	6330	3	US-09-880-427-2
14	13	100.0	6330	3	US-09-306-538B-2
15	13	100.0	8801	4	US-09-949-016-1791
16	13	100.0	8801	4	US-09-949-016-1791
17	13	100.0	16427	4	US-09-902-540-11601
18	13	100.0	36791	4	US-09-949-016-17451
19	13	100.0	248968	4	US-09-949-016-17451
20	12.6	96.9	21	4	US-09-949-016-18061
21	12	92.3	69	4	US-09-657-472-1254
22	12	92.3	69	4	US-08-956-171B-2195
23	12	92.3	319	1	US-08-781-986A-2195
24	12	92.3	319	1	US-08-592-126-126
25	12	92.3	319	1	US-09-168-595-126
26	12	92.3	462	4	US-09-248-796A-12389
27	12	92.3	510	3	US-09-291-922-11
28	12	92.3	601	4	US-09-949-016-25035

28 12 92.3 601 4 US-09-949-016-63994 Sequence 63994, A
29 12 92.3 601 4 US-09-949-016-71051 Sequence 71051, A
30 12 92.3 601 4 US-09-949-016-71052 Sequence 71052, A
31 12 92.3 601 4 US-09-949-016-81626 Sequence 81626, A
32 12 92.3 601 4 US-09-949-016-132437 Sequence 132437, A
33 12 92.3 601 4 US-09-949-016-196206 Sequence 196206, A
34 12 92.3 625 3 US-08-998-416-138 Sequence 138, App
35 12 92.3 672 3 US-09-134-001C-1570 Sequence 1570, App
36 12 92.3 870 4 US-09-844-497-1 Sequence 1, Appli
37 12 92.3 1041 1 US-08-213-403-1 Sequence 1, Appli
38 12 92.3 1041 1 US-08-458-077-1 Sequence 1, Appli
39 12 92.3 1041 1 US-08-460-741-1 Sequence 1, Appli
40 12 92.3 1041 1 US-08-747-240-1 Sequence 1, Appli
41 12 92.3 1041 4 US-09-039-642B-1 Sequence 1, Appli
42 12 92.3 1041 4 US-09-107-532A-1769 Sequence 1769, App
43 12 92.3 1194 4 US-09-252-991A-13276 Sequence 13276, A
44 12 92.3 1268 4 US-09-270-767-30816 Sequence 30816, A
45 12 92.3 1305 4 US-09-252-991A-12685 Sequence 12685, A

ALIGNMENTS

RESULT 1
US-09-973-132-5
; Sequence 5, Application US/09973132
; Patent No. 6593092
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687.US.P1
; CURRENT APPLICATION NUMBER: US/09/973,132
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragments
US-09-973-132-5

Query Match 100.0%; Score 13; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. NO. 2.2e-02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCAATGGAAGCC 13
Db 1 CCCAATGGAAGCC 13

RESULT 2
US-09-973-132-8
; Sequence 8, Application US/09973132
; Patent No. 6593092
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687.US.P1
; CURRENT APPLICATION NUMBER: US/09/973,132
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragments
US-09-973-132-8

Query Match      100.0%; Score 13; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
    |||||
Db 9 CCCAATGGAAGCC 21

RESULT 3
US-09-973-132-9/c
; Sequence 9, Application US/09973132
; Patent No. 6593092
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687 US P1
; CURRENT APPLICATION NUMBER: US/09/973,132
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragments
US-09-973-132-9

Query Match      100.0%; Score 13; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
    |||||
Db 21 CCCAATGGAAGCC 9

RESULT 4
US-09-621-976-14538/c
; Sequence 14538, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 14538
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-14538

Query Match      100.0%; Score 13; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
    |||||
Db 312 CCCAATGGAAGCC 300

; ORGANISM: Artificial Sequence
; Sequence 18501, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18501
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-18501/c

Query Match      100.0%; Score 13; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
    |||||
Db 535 CCCAATGGAAGCC 523

RESULT 5
US-09-949-016-18501/c
; Sequence 18501, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18501
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-18501/c

Query Match      100.0%; Score 13; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
    |||||
Db 535 CCCAATGGAAGCC 523

RESULT 6
US-09-949-016-103791/c
; Sequence 103791, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103791
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-103791/c

Query Match      100.0%; Score 13; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
    |||||
Db 535 CCCAATGGAAGCC 523

RESULT 7
US-09-949-016-153904/c
; Sequence 153904, Application US/09949016
```

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 153904
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-153904

Query Match 100.0%; Score 13; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
|||||
DB 316 CCCAATGGAAGCC 304

RESULT 8
US-09-949-016-153905/c
Sequence 153905, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 153905
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-153905

Query Match 100.0%; Score 13; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
|||||
DB 229 CCCAATGGAAGCC 217

RESULT 9
US-09-902-540-3385
Sequence 3385, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 3385
LENGTH: 1014
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-3385

Query Match 100.0%; Score 13; DB 4; Length 1014;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
|||||
DB 633 CCCAATGGAAGCC 645

RESULT 10
US-09-214-916A-1
Sequence 1, Application US/09214916A
Patent No. 6673585
GENERAL INFORMATION:
APPLICANT: QUERRELOU, JOEL
APPLICANT: CAMBON, MARIE ANNE
TITLE OF INVENTION: Heat-Stable DNA polymerase of Archaeobacteria of the genus " Pyr
TITLE OF INVENTION: SP"
FILE REFERENCE: A2B10PCT-US April 2001
CURRENT APPLICATION NUMBER: US/09/214,916A
CURRENT FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: FR96/08631
PRIOR FILING DATE: 1996-07-10
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 4446
TYPE: DNA
ORGANISM: archaeobacteria pyrococcus
FEATURE:
NAME/KEY: CDS
LOCATION: (1547)..(3862)
NAME/KEY: stop codon
LOCATION: (3860)..(3862)
US-09-214-916A-1

Query Match 100.0%; Score 13; DB 4; Length 4446;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
|||||
DB 2527 CCCAATGGAAGCC 2539

RESULT 11
US-09-293-170-4
Sequence 4, Application US/09293170
Patent No. 6383777
GENERAL INFORMATION:
APPLICANT: Breyer, Richard M.
APPLICANT: Ma, Lijun
APPLICANT: Kennedy, Chris
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH YIELD
PRODUCTION OF EUKARYOTIC PROTEINS
TITLE OF INVENTION: PRODUCTION OF EUKARYOTIC PROTEINS
FILE REFERENCE: 22000.0094
CURRENT APPLICATION NUMBER: US/09/293,170
CURRENT FILING DATE: 1999-04-16
EARLIER APPLICATION NUMBER: 60/081,989

```
Query Match 100.0%; Score 13; DB 3; Length 6330;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 C C C A A T G G A A G C C 13
|||
Db 633 C C C A A T G G A A G C C 645

```

RESULT 14
US-09-949-016-11791/c
; Sequence 11791, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 11791
; LENGTH: 8801
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(8801)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11791

```

```
Query Match      100.0%; Score 13; DB 4; Length 8801;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 CCCAATGGAAGCC 13
|||
Db 2873 CCCAATGGAAGCC 28

```

RESULT 15
US-09-949-016-14615/c
; Sequence 14615, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

```



```

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14615
; LENGTH: 8801
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(8801)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14615

```

```

Query Match      100.0%; Score 13; DB 4; Length 8801;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  CCCAATGGAAGCC 13
        |||||
Db      2873 CCCAATGGAAGCC 2861

```

```

Search completed: August 7, 2005, 11:52:21
Job time : 47.6818 secs

```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2005, 11:37:03 ; Search time 243.455 Seconds
(without alignments)
346.144 Million cell updates/sec

Title: US-09-542-718-5
Perfect score: 13
Sequence: 1 cccaatggaagcc 13

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	13	100.0	13	9	US-09-973-132-5
2	13	100.0	25	21	US-10-719-900-760038
3	13	100.0	29	9	US-09-973-132-8
4	13	100.0	29	9	US-09-973-132-9
5	13	100.0	40	10	US-09-823-257A-9
6	13	100.0	40	21	US-10-995-812-9
7	13	100.0	51	20	US-10-865-478-355

c 8	13	100.0	108	19	US-10-437-963-23271	Sequence 23271, A
c 9	13	100.0	153	18	US-10-424-599-50341	Sequence 50341, A
c 10	13	100.0	164	18	US-10-424-599-107397	Sequence 107397, A
c 11	13	100.0	165	19	US-10-437-963-71682	Sequence 71682, A
c 12	13	100.0	201	21	US-10-741-600-54721	Sequence 54721, A
c 13	13	100.0	201	21	US-10-741-600-54722	Sequence 54722, A
c 14	13	100.0	201	21	US-10-741-600-55166	Sequence 55166, A
c 15	13	100.0	201	21	US-10-741-600-55186	Sequence 55186, A
c 16	13	100.0	227	9	US-09-796-692-5714	Sequence 5714, Ap
c 17	13	100.0	227	14	US-10-040-852-5714	Sequence 5714, Ap
c 18	13	100.0	227	17	US-10-057-475B-5714	Sequence 5714, Ap
c 19	13	100.0	227	17	US-10-154-884B-5714	Sequence 5714, Ap
c 20	13	100.0	227	19	US-10-764-324-5714	Sequence 5714, Ap
c 21	13	100.0	258	19	US-10-767-701-17706	Sequence 17706, A
c 22	13	100.0	393	18	US-10-424-599-62759	Sequence 62759, A
c 23	13	100.0	400	17	US-10-242-535A-8383	Sequence 8383, Ap
c 24	13	100.0	400	18	US-10-085-783A-8383	Sequence 8383, Ap
c 25	13	100.0	405	14	US-10-060-036-582	Sequence 582, App
c 26	13	100.0	421	18	US-10-424-599-44907	Sequence 44907, A
c 27	13	100.0	424	10	US-09-918-995-4110	Sequence 4110, Ap
c 28	13	100.0	433	20	US-10-425-115-131946	Sequence 131946, A
c 29	13	100.0	443	10	US-09-814-353-581	Sequence 581, Ap
c 30	13	100.0	443	10	US-09-814-353-5915	Sequence 8915, Ap
c 31	13	100.0	444	19	US-10-437-963-69721	Sequence 69721, A
c 32	13	100.0	450	19	US-10-021-323-13095	Sequence 13095, A
c 33	13	100.0	450	20	US-10-425-115-30242	Sequence 30242, A
c 34	13	100.0	483	10	US-09-918-995-36881	Sequence 36881, A
c 35	13	100.0	487	9	US-09-747-155-176	Sequence 176, App
c 36	13	100.0	509	19	US-10-437-963-81242	Sequence 81242, A
c 37	13	100.0	531	13	US-10-027-632-269358	Sequence 269358, A
c 38	13	100.0	531	17	US-10-027-632-269358	Sequence 269358, A
c 39	13	100.0	551	9	US-09-864-761-23612	Sequence 23612, A
c 40	13	100.0	579	18	US-10-424-599-93218	Sequence 93218, A
c 41	13	100.0	595	9	US-09-864-761-6879	Sequence 6879, Ap
c 42	13	100.0	597	13	US-10-027-632-212127	Sequence 212127, A
c 43	13	100.0	597	17	US-10-027-632-212127	Sequence 212127, A
c 44	13	100.0	600	22	US-10-972-079-26711	Sequence 26711, A
c 45	13	100.0	600	22	US-10-972-079-26712	Sequence 26712, A

ALIGNMENTS

RESULT 1
US-09-973-132-5
; Sequence 5, Application US/09973132
; Patent No. US20020137069A1
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; APPLICANT: Merchant, B.T.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687.US.P1
; CURRENT APPLICATION NUMBER: US/09/973,132
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragments
US-09-973-132-5

Query Match 100.0%; Score 13; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
| | | | | | | | | | | | | | |
Db 1 CCCAATGGAAGCC 13

```
RESULT 2
US-10-719-900-760038
; Sequence 760038, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 760038
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-760038

Query Match 100.0%; Score 13; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
Db 9 CCCAATGGAAGCC 21

RESULT 3
US-09-973-132-8
; Sequence 8, Application US/09973132
; Patent No. US20020137069A1
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; APPLICANT: Merchant, B.T.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687.US.P1
; CURRENT APPLICATION NUMBER: US/09/973,132
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragments
US-09-973-132-8

Query Match 100.0%; Score 13; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
Db 9 CCCAATGGAAGCC 21

RESULT 4
US-09-973-132-9/c
; Sequence 9, Application US/09973132
; Patent No. US20020137069A1
; GENERAL INFORMATION:
; APPLICANT: Wu, H.
; APPLICANT: Merchant, B.T.
; TITLE OF INVENTION: BETA-2 ADRENERGIC POLYMORPHISM DETECTION
; FILE REFERENCE: 6687.US.P1
; CURRENT APPLICATION NUMBER: US/09/973,132
```

```
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 09/542,718
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic fragments
US-09-973-132-9

Query Match 100.0%; Score 13; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
Db 21 CCCAATGGAAGCC 9

RESULT 5
US-09-823-257A-9
; Sequence 9, Application US/09823257A
; Publication No. US20030096231A1
; GENERAL INFORMATION:
; APPLICANT: Landers, John
; TITLE OF INVENTION: High Throughput Methods for Haplotyping
; FILE REFERENCE: P0715/7003 (HCL)
; CURRENT APPLICATION NUMBER: US/09/823,257A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/194,425
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Human Oligonucleotide
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: amino group attached
US-09-823-257A-9

Query Match 100.0%; Score 13; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
Db 26 CCCAATGGAAGCC 38

RESULT 6
US-10-995-812-9
; Sequence 9, Application US/10995812
; Publication No. US20050089920A1
; GENERAL INFORMATION:
; APPLICANT: Landers, John
; TITLE OF INVENTION: High Throughput Methods for Haplotyping
; FILE REFERENCE: P0715.70003US01
; CURRENT APPLICATION NUMBER: US/10/995,812
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 09/823,257
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/194,425
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
```

;
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Human Oligonucleotide
; NAME/KEY: misc.feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: amino group attached
US-10-995-812-9

Query Match 100.0%; Score 13; DB 21; Length 40;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
| | | | | | | | | |
Db 26 CCCAATGGAAGCC 38

RESULT 7
US-10-865-478-355
; Sequence 355, Application US/10865478
; Publication No. US20040235041A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: cSingle Nucleotide Polymorphisms for Known Genes
; FILE REFERENCE: 15966-534-CIP1
; CURRENT APPLICATION NUMBER: US/10/865,478
; CURRENT FILING DATE: 2004-06-10
; PRIOR APPLICATION NUMBER: 60/109,024
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: 09/443,199
; PRIOR FILING DATE: 1993-11-16
; PRIOR APPLICATION NUMBER: 09/442,129
; PRIOR FILING DATE: 1993-11-16
; PRIOR APPLICATION NUMBER: 09/442,849
; PRIOR FILING DATE: 1993-11-17
; NUMBER OF SEQ ID NOS: 880
; SOFTWARE: Curagen Patent Formatter Version 0.9
; SEQ ID NO 355
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: (26)...(0)
; OTHER INFORMATION: single nucleotide polymorphism
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Accession number cg43040273
US-10-865-478-355

Query Match 100.0%; Score 13; DB 20; Length 51;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
| | | | | | | | | |
Db 20 CCCAATGGAAGCC 32

RESULT 8
US-10-437-963-23271/c
; Sequence 23271, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 23271
; LENGTH: 108
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_28367C.1
US-10-437-963-23271

Query Match 100.0%; Score 13; DB 19; Length 108;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
| | | | | | | | | |
Db 28 CCCAATGGAAGCC 16

RESULT 9
US-10-424-599-50341/c
; Sequence 50341, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 50341
; LENGTH: 153
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_16468C.1
US-10-424-599-50341

Query Match 100.0%; Score 13; DB 18; Length 153;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
| | | | | | | | | |
Db 59 CCCAATGGAAGCC 47

RESULT 10
US-10-424-599-107397/c
; Sequence 107397, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 107397
; LENGTH: 164
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_67995C.1
US-10-424-599-107397

Query Match 100.0%; Score 13; DB 18; Length 164;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
| | | | | | | | | | | | | | |
DB 66 CCCAATGGAAGCC 54

RESULT 11
US-10-437-963-71682/c
; Sequence 71682, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 71682
; LENGTH: 165
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72132C.1
US-10-437-963-71682

Query Match 100.0%; Score 13; DB 19; Length 165;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
| | | | | | | | | | | | | | |
DB 70 CCCAATGGAAGCC 58

RESULT 12
US-10-741-600-54721/c
; Sequence 54721, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54721
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-54721

Query Match 100.0%; Score 13; DB 21; Length 201;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
| | | | | | | | | | | | | | |
DB 29 CCCAATGGAAGCC 17

RESULT 13
US-10-741-600-54722/c
; Sequence 54722, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54722
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-54722

Query Match 100.0%; Score 13; DB 21; Length 201;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
| | | | | | | | | | | | | | |
DB 116 CCCAATGGAAGCC 104

RESULT 14
US-10-741-600-55166
; Sequence 55166, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55166
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-55166

Query Match 100.0%; Score 13; DB 21; Length 201;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCAATGGAAGCC 13
| | | | | | | | | | | | | | |
DB 86 CCCAATGGAAGCC 98

RESULT 15
US-10-741-600-55186
; Sequence 55186, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55186
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-55186

Query Match 100.0%; Score 13; DB 21; Length 201;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55186
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-55186
```

```
Query Match      100.0%; Score 13; DB 21; Length 201;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCCAATGGAAGCC 13
        |||||
Db      173 CCCAATGGAAGCC 185
```

```
Search completed: August 7, 2005, 15:40:01
Job time : 245.455 secs
```

This Page Blank (uspto)